

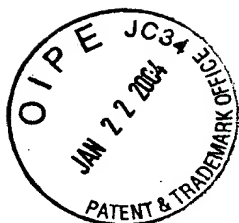


Neutrokin- $\alpha$

1 AAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTGCCATGTAGTGCACGCAGGAC 60  
61 ATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGTCACTTATTCTAAAGGCC 120  
121 CCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAGGGAGCAGTCACGCC 180  
1 M D D S T E R E Q S R L 12  
181 TTA CT TCT TGC CTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGTTTCCATCCTCC 240  
13 T S C L K K R E E M K L K E C V S I L P 32  
CD-I  
241 CACGGAAGGAAAGCCCTCTGTCCGATCCTCAAAGACGGAAAGCTGCTGGCTGCAACCT 300  
33 R K E S P S V R S S K D G K L L A A T L 52  
CD-I  
301 TGCTGCTGGCACTGCTGTCTTGCTGCCTCACGGTGGTGTCTTTCTACCAGGTGGCCGCC 360  
53 L L A L L S C C L T V V S F Y Q V A A L 72  
361 TGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGC 420  
73 Q G D L A S L R A E L Q G H H A E K L P 92  
CD-II  
421 CAGCAGGAGCAGGAGCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGAC 480  
93 A G A G A P K A G L E E A P A V T A G L 112  
CD-III  
#  
481 TGAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAATA 540  
113 K I F E P P A P G E G N S S Q N S R N K 132  
541 AGCGTGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAG 600  
133 R A V Q G P E E T V T Q D C L Q L I A D 152  
CD-IV

FIG.1A

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Neutrokin- $\alpha$

601 ACAGTGAAACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCT 660  
153 S E T P T I Q K G S Y T F V P W L L S F 172  
CD-V

661 TTAAAAGGGGAAGTGCCCTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTT 720  
173 K R G S A L E E K E N K I L V K E T G Y 192  
CD-V CD-VI

721 ACTTTTTTATATATGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAA 780  
193 F F I Y G Q V L Y T D K T Y A M G H L I 212  
CD-VI CD-VII

781 TTCAGAGGAAGAAGGTCCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGAT 840  
213 Q R K K V H V F G D E L S L V T L F R C 232  
CD-VII CD-VIII

#  
841 GTATTCAAATATGCCTGAAACACTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAA 900  
233 I Q N M P E T L P N N S C Y S A G I A K 252  
CD-VIII CD-IX

901 AACTGGAAGAAGGAGATGAACTCCAACCTTGCAATACCAAGAGAAAATGCACAAATATCAC 960  
253 L E E G D E L Q L A I P R E N A Q I S L 272  
CD-X

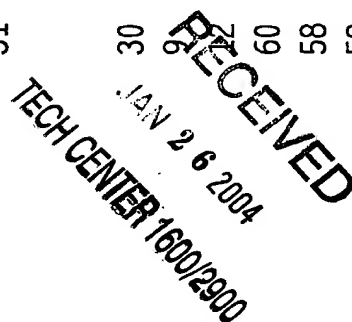
961 TGGATGGAGATGTCACATTTTTTGGTGCATTGAACTGCTGTGACCTACTTACACCATGT 1020  
273 D G D V T F F G A L K L L 285  
CD-XI

1021 CTGTAGCTATTTTCCTCCCTTTCTCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATA 1080

1081 CCAAAAAAAAAAAAAAAAAA 1100

FIG.1B

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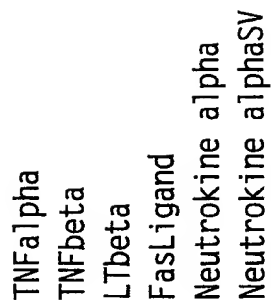
		10	20	30	TNFalpha TNFbeta LTbeta FasLigand Neutrokine alpha Neutrokine alphaSV
1	MSTESMIRDVEL	- - - - -	- - - - -	- AEEA	
1	M - - - - -	- - - - -	- - - - -	TPPERL	
1	MGA - - - - -	- - - - -	- - - - -	- - - - -	
1	MQQPFNYPYPIYW	- VDS	SASSPWAPP	GTV	
1	MDDSTEREQSRLL	TSC	LKKREEMKL	KECVSI	
1	MDDSTEREQSRLL	TSC	LKKREEMKL	KECVSI	

		40	50	60	TNFalpha TNFbeta LTbeta FasLigand Neutrokine alpha Neutrokine alphaSV
17	LPKKTGGPQ	- GSRR	- - - - -	- - - - -	
8	F - - - - -	- - - - -	- - - - -	- - - - -	
4	- - - LGLEGRGG	- - - - -	- - - - -	- - - - -	
30	LPCTSVPRRPG	QRPPPPPPPP	PLPPP	PLPPP	
31	LPRKESSPSVRSSKD	- - GKLLAAAT	LLALL	LLALL	
31	LPRKESSPSVRSSKD	- - GKLLAAAT	LLALL	LLALL	

		70	80	90	TNFalpha TNFbeta LTbeta FasLigand Neutrokine alpha Neutrokine alphaSV
30	- - - - -	- - - - C	LFLLSLFS	- - - - -	
9	- - - - -	LP RVRGTTTLH	LLGLLVLLLP	- - - - -	
57	- - - - -	- RLQGRGSLL	LAVAGATSLVT	- - - - -	
60	PPPLPPLPLPPLPKRG	NHSTGLCL	LLVMFFFM	- - - - -	
58	SCCLTVVSFYQVAALQ	GDLASLRAE	LQGHH	- - - - -	
58	SCCLTVVSFYQVAALQ	GDLASLRAE	LQGHH	- - - - -	



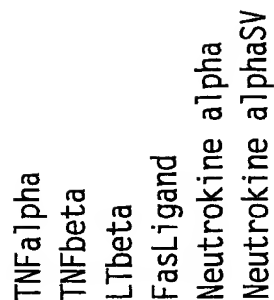
	100										110										120										
38	F	L	-	-	I	V	A	G	A	T	T	L	F	C	L	L	H	F	G	V	I	G	P	Q	R	E	E	F	F	P	R
31	G	A	Q	Q	L	P	G	V	G	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
32	L	L	L	A	V	P	I	T	V	L	A	V	L	A	L	V	P	Q	D	Q	G	G	L	V	T	E	E	T	A	D	P
90	V	L	V	A	L	V	G	L	G	L	G	M	F	Q	L	F	H	L	Q	K	E	L	A	E	L	R	E	S	T	S	-
88	A	E	K	L	P	A	G	A	G	A	P	K	A	G	L	E	E	E	A	P	A	V	T	A	G	L	K	I	F	E	P
88	A	E	K	L	P	A	G	A	G	A	P	K	A	G	L	E	E	E	A	P	A	V	T	A	G	L	K	I	F	E	P

	130										140										150									
66	D	L	S	L	I	S	-	P	L	A	-	Q	A	V	R	S	S	R	T	P	S	D	-	-	-	K	P	V	A	
41	-	-	-	T	P	S	-	A	A	Q	-	T	A	R	Q	H	P	K	M	H	L	A	H	S	T	L	K	P	A	A
62	G	A	Q	A	Q	Q	-	G	L	G	F	Q	K	L	P	E	E	E	P	E	T	D	L	S	P	G	L	P	A	A
120	Q	M	H	T	A	S	-	S	L	E	-	K	Q	I	G	H	P	S	P	P	P	E	K	K	E	L	R	K	V	A
118	P	A	P	G	E	G	N	S	S	Q	N	S	R	N	K	R	A	V	Q	G	P	E	E	T	V	T	Q	D	C	L
118	P	A	P	G	E	G	N	S	S	Q	N	S	R	N	K	R	A	V	Q	G	P	E	E	T	-	-	-	-	-	-

	160	170	180
91	H V V A N P Q A E G - Q	- - - - - L Q W L N R R A N A L L	
66	H I I G D P S K Q N - S	- - - - - L L W R A N T D R A F L	
91	H I I G A P L K - G Q G	- - - - - L G W E T J K E Q A F L	
148	H L T G K S N S R S M P	- - - - - L E W E D J Y G I V L L	
148	Q L I A D S E T P T I Q	K G S Y T F V P W L - - - L S F K	
142	- - - - -	G S Y T F V P W L - - - L S F K	

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**FIG. 2B**

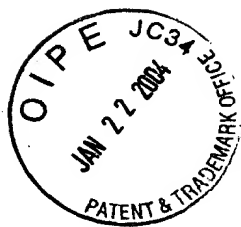


TNFalpha  
TNFbeta  
LTbeta  
FasLigand  
Neutrokin alpha  
Neutrokin alphaSV

TNFalpha  
TNFbeta  
LTbeta  
FasLigand  
Neutrokinine alpha  
Neutrokinine alphaSV

FIG. 2C

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		280		290		300																									
193	P	I	Y	L	G	G	V	F	Q	L	E	K	G	D	R	L	S	A	E	I	N	R	P	D	Y	L	D	F	A	E	TNFalpha
166	S	M	Y	H	G	A	A	F	Q	L	T	Q	G	D	Q	L	S	T	H	T	D	G	I	P	H	L	V	L	S	P	TNFbeta
204	S	V	G	F	G	G	L	V	Q	L	R	R	G	E	R	V	Y	V	N	I	S	H	P	D	M	V	D	F	A	R	LTbeta
242	S	S	Y	L	G	A	V	F	N	L	T	S	A	D	H	L	T	V	N	V	S	E	L	S	L	V	N	F	E	E	FasLigand
244	S	C	Y	S	A	G	I	A	K	L	E	E	G	D	E	L	Q	L	A	I	P	R	E	N	A	Q	I	S	L	D	Neutrokinine alpha
225	S	C	Y	S	A	G	I	A	K	L	E	E	G	D	E	L	Q	L	A	I	P	R	E	N	A	Q	I	S	L	D	Neutrokinine alphaSV

		310											
223	S	G	Q	V	Y	F	G	I	I	A	L	TNFalpha	
196	S	-	T	V	F	F	G	A	F	A	L	TNFbeta	
234	-	G	K	T	F	F	G	A	V	M	V	G	LTbeta
272	S	-	Q	T	F	F	G	L	Y	K	L	FasLigand	
274	G	D	V	T	F	F	G	A	L	K	L	Neutrokinine alpha	
255	G	D	V	T	F	F	G	A	L	K	L	Neutrokinine alphaSV	

FIG.2D

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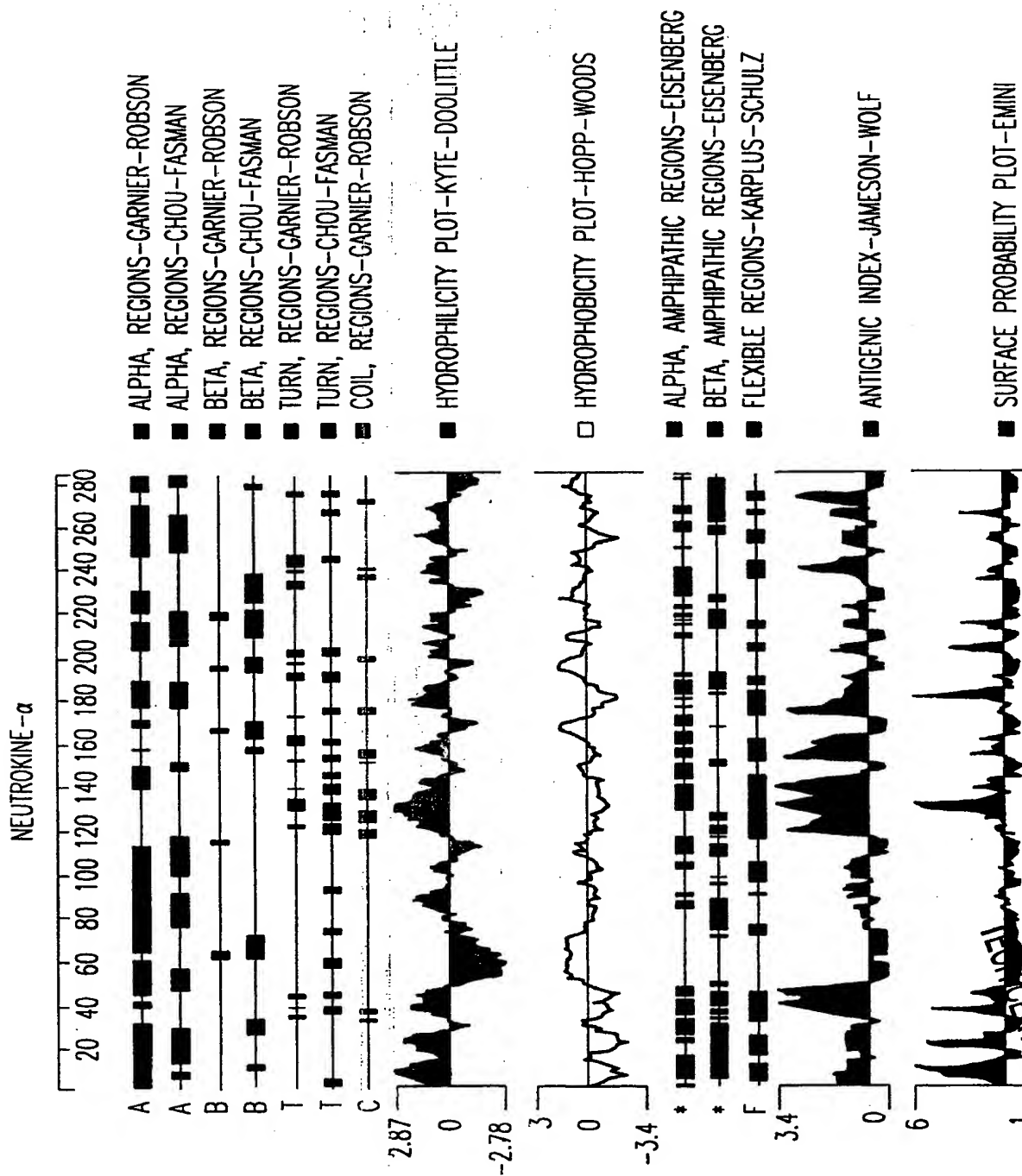
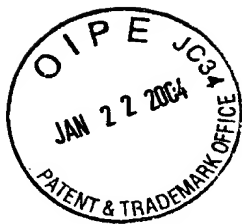


FIG.3

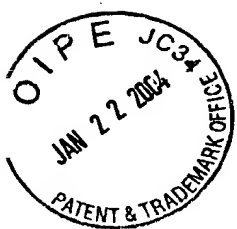


	1				50
HSOAD55R	.....A	GGNTAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HNEDU15X	...AAATTCA	GGATAACTCT	CCTGAGGGGT	GAGCCAAGCC	CTGCCATGTA
HSLAH84R	.AATTCGGCA	NAGNAACTG	GTTACTTTT	TATATATGGT	CAGGTTTTAT
HLTBM08R	AATTCGGCAC	GAGCAAGGCC	GGCCTGGAGG	AAGCTCCAGC	TGTCACCGCG
	51				100
HSOAD55R	GTGCACGCAG	GACATCANCA	A..ACACANN	NNNCAGGAAA	TAATCCATTTC
HNEDU15X	GTGCACGCAG	GACATCAACA	A..ACACAGA	TAACAGGAAA	TGATCCATTTC
HSLAH84R	ATACTGATAA	GACCTACGCC	ATGGGACATC	TAGTTCAGAG	GAAGAAGGTC
HLTBM08R	GGACTGAAAA	TCTTTGAACC	ACCAGCTCCA	GGAGAAGGCA	ACTCCAGTCA
	101				150
HSOAD55R	CCTGTGGTCA	CTTATTCTAA	AGGCCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HNEDU15X	CCTGTGGTCA	CTTATTCTAA	AGGCCCCAAC	CTTCAAAGTT	CAAGTAGTGA
HSLAH84R	CATGTCTTTG	GGGATGAATT	GAGTCTGGTG	ACTTTGTTTC	GATGTATTCA
HLTBM08R	GAACAGCAGA	AATAAGCGTG	CCGTTTCAGG	TCCAGAAGAA	ACAGTCACTC
	151				200
HSOAD55R	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HNEDU15X	TATGGATGAC	TCCACAGAAA	GGGAGCAGTC	ACGCCTTACT	TCTTGCCTTA
HSLAH84R	AAATATGCCT	GAAACACTAC	CCAATAATTC	CTGCTATTCA	GCTGGCATTG
HLTBM08R	AAGACTGCTT	GCAACTGNNT	GCAGACAGTG	AAACACCAAC	TATACAAAAA
	201				250
HSOAD55R	AGAAAAGAGA	AGAAATGAAA	CTGNAAGGAG	TGTGTTTCCA	TCCTCCCACG
HNEDU15X	AGAAAAGAGA	AGAAATGAAA	CT.GAAGGAG	TGTGTTTCCA	TCCTCCCACG
HSLAH84R	CAAACTGGN	AGGAAGGA..	...GATGAAC	TCCAAC TTGC	AATACCAGGG
HLTBM08R	GGCTCCCTTC	TGNTGCCACA	TTTGGGCCAA	GGAATGGAGA	GATTTCTTCG
	251				300
HSOAD55R	GAAGGAAAGC	CCCTCTNTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HNEDU15X	GAAGGAAAGC	CCCTCTGTCC	GATCCTCCAA	AGACGGAAAG	CTGCTGGCTG
HSLAH84R	GAAAATGCAC	AATTATCACT	GGGATGGAGA	TGTTACATT	TTTTGGGTGC
HLTBM08R	TCTGGAAACA	TTTTGCCAAA	CTCTTCAGAT	ACTCTTTNCT	CTCTGGGAAT
	301				350
HSOAD55R	CAACCTTGNT	GNTGACATTG	TGTTCTTGCT	GNCTCAAGGT	GGTGTTNTT.
HNEDU15X	CAACCTTGCT	GCTGGCACTG	CTGTCTTGCT	GCCTCACGGT	GGTGCTTTTC
HSLAH84R	CATTGAAACT	GCTGTGACCT	NCTTACANCA	NGTGCTGTTN	GCTATTTTNC
HLTBM08R	CAAAGGAAAA	TCTCTACTTA	GATTNACACA	TTTGTTCCCA	TGGGTNTCTT
	351				400
HSOAD55R	.....	.....	.....	.....	.....
HNEDU15X	TACCAGGTGG	CCGCCCTGCA	AGGGGACCTG	GCCAGCCTCC	GGGCAGAGCT
HSLAH84R	CTNCCTNTTG	TNTGGTAACC	TCTTAGGAAG	GAAGGATTCT	TAAGTGGGAA
HLTBM08R	AAGTTTTTAA	AGGGGAGTGC	CCTTAGGAGG	AAAAGGGGAT	AAATATTGGC

FIG.4A

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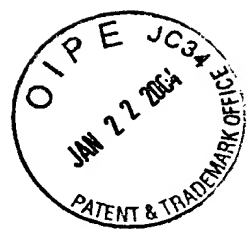




	401		450
HSOAD55R	.....	.....	.....
HNEDU15X	GCAGGGCCAC	CACGCGGAGA	AGCTGCCAGC
HSLAH84R	ATAACCCAAA	AAAANNTTAA	ANGGGTANGN
HLTBM08R	CAAGGNACTG	GTTANTTTNT	AAATATGGTC
		AGGTTTNTAT	ANCTGGTAGG
	451		500
HSOAD55R	.....	.....	.....
HNEDU15X	CCGGCCTGGA	GGAAGCTCCA	GCTGTCACCG
HSLAH84R	CNNGNNGNNT	TTTNGGNNTA	TNTTNTNNTN
HLTBM08R	CCTCGCCATG	GGCATTNATT	CANGGNGAGG
		NCNNTCTTTT	GGGNTGA...
	501		550
HSOAD55R	.....	.....	.....
HNEDU15X	CCACCAGCTC	CAGGAGAAGG	CAACTCCAGT
HSLAH84R	CNANGGGGGN	TTTTT.....	.....
HLTBM08R	.....	.....	.....
	551		600
HSOAD55R	.....	.....	.....
HNEDU15X	TGCCGTTTCA	GGTCCAGAAG	AAACAGTCAC
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	601		650
HSOAD55R	.....	.....	.....
HNEDU15X	TTGCAGACAG	TGAAACACCA	ACTATACAAA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	651		700
HSOAD55R	.....	.....	.....
HNEDU15X	CCATGGCTTC	TCAGCTTTAA	AAGGGGAAGT
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	701		750
HSOAD55R	.....	.....	.....
HNEDU15X	TAAAATATTG	GTCAAAGAAA	CTGGTTACTT
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	751		800
HSOAD55R	.....	.....	.....
HNEDU15X	TATATACTGA	TAAGACCTAC	GCCATGGGAC
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....

FIG.4B

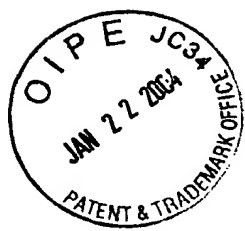
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	801		850
HSOAD55R	.....	.....	.....
HNEDU15X	GTCCATGTCT	TTGGGGATGA	ATTGAGTCTG GTGACTTTGT TTCGATGTAT
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	851		900
HSOAD55R	.....	.....	.....
HNEDU15X	TCAAAATATG	CCTGAAACAC	TACCCAATAA TTCCTGCTAT TCAGCTGGCA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	901		950
HSOAD55R	.....	.....	.....
HNEDU15X	TTGCAAAACT	GGAAGAAGGA	GATGAACTCC AACTTGCAAT ACCAAGAGAA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	951		1000
HSOAD55R	.....	.....	.....
HNEDU15X	AATGCACAAA	TATCACTGGA	TGGAGATGTC ACATTTTTTG GTGCATTGAA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	1001		1050
HSOAD55R	.....	.....	.....
HNEDU15X	ACTGCTGTGA	CCTACTTACA	CCATGTCTGT AGCTATTTTC CTCCCTTTCT
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	1051		1100
HSOAD55R	.....	.....	.....
HNEDU15X	CTGTACCTCT	AAGAAGAAAG	AATCTAACTG AAAATACCAA AAAAAAAAAA
HSLAH84R	.....	.....	.....
HLTBM08R	.....	.....	.....
	1101		
HSOAD55R	.....		
HNEDU15X	AAAAAA		
HSLAH84R	.....		
HLTBM08R	.....		

FIG.4C

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Neutrokin- $\alpha$ SV

1 ATGGATGACTCCACAGAAAGGGAGCAGTCACGCCTTACTTCTTGCCTTAAGAAAAGAGAA 60  
1 M D D S T E R E Q S R L T S C L K K R E 20

61 GAAATGAAACTGAAGGAGTGTGTTTCCATCCTCCCACGGAAGGAAAGCCCTCTGTCCGA 120  
21 E M K L K E C V S I L P R K E S P S V R 40  
CD-I

121 TCCTCCAAAGACGGAAAGCTGCTGGCTGCAACCTTGCTGCTGGCACTGCTGTCTTGCTGC 180  
41 S S K D G K L L A A T L L L A L L S C C 60  
CD-I

181 CTCACGGTGGTGTCTTTCTACCAGGTGGCCGCCCTGCAAGGGGACCTGGCCAGCCTCCGG 240  
61 L T V V S F Y Q V A A L Q G D L A S L R 80  
CD-II

241 GCAGAGCTGCAGGGCCACCACGCGGAGAAGCTGCCAGCAGGAGCAGGAGCCCCAAGGCC 300  
81 A E L Q G H H A E K L P A G A G A P K A 100  
CD-II CD-III

301 GGCCTGGAGGAAGCTCCAGCTGTCACCGCGGGACTGAAAATCTTTGAACCACCAGCTCCA 360  
101 G L E E A P A V T A G L K I F E P P A P 120  
CD-III

#

361 GGAGAAGGCAACTCCAGTCAGAACAGCAGAAATAAGCGTGCCGTTCAAGGTCCAGAAGAA 420  
121 G E G N S S Q N S R N K R A V Q G P E E 140

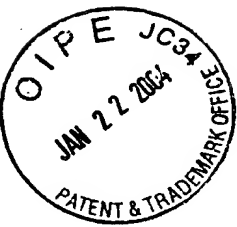
421 ACAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGGAAGTGCCCTAGAA 480  
141 T G S Y T F V P W L L S F K R G S A L E 160  
CD-IV

481 GAAAAAGAGAATAAAATATTGGTCAAAGAACTGGTTACTTTTTTATATATGGTCAGGTT 540  
161 E K E N K I L V K E T G Y F F I Y G Q V 180  
CD-IV CD-V

541 TTATATACTGATAAGACCTACGCCATGGGACATCTAATTCAGAGGAAGAAGGTCCATGTC 600  
181 L Y T D K T Y A M G H L I Q R K K V H V 200  
CD-VI CD-VII

FIG.5A

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Neutrokin-αSV

601 TTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAATATGCCTGAAACA 660  
201 F G D E L S L V T L F R C I Q N M P E T 220  
CD-VIII CD-VIII

661 CTACCCAATAATTCCTGCTATTTCAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACTC 720  
221 L P N N S C Y S A G I A K L E E G D E L 240  
CD-IX CD-X

721 CAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTT 780  
241 Q L A I P R E N A Q I S L D G D V T F F 260  
CD-X CD-XI

781 GGTGCATTGAACTGCTGTGACCTACTTACACCATGTCTGTAGCTATTTTCCTCCCTTTC 840  
261 G A L K L L 266  
CD-XI

841 TCTGTACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAAAAA 900

901 AAA 903

FIG.5B

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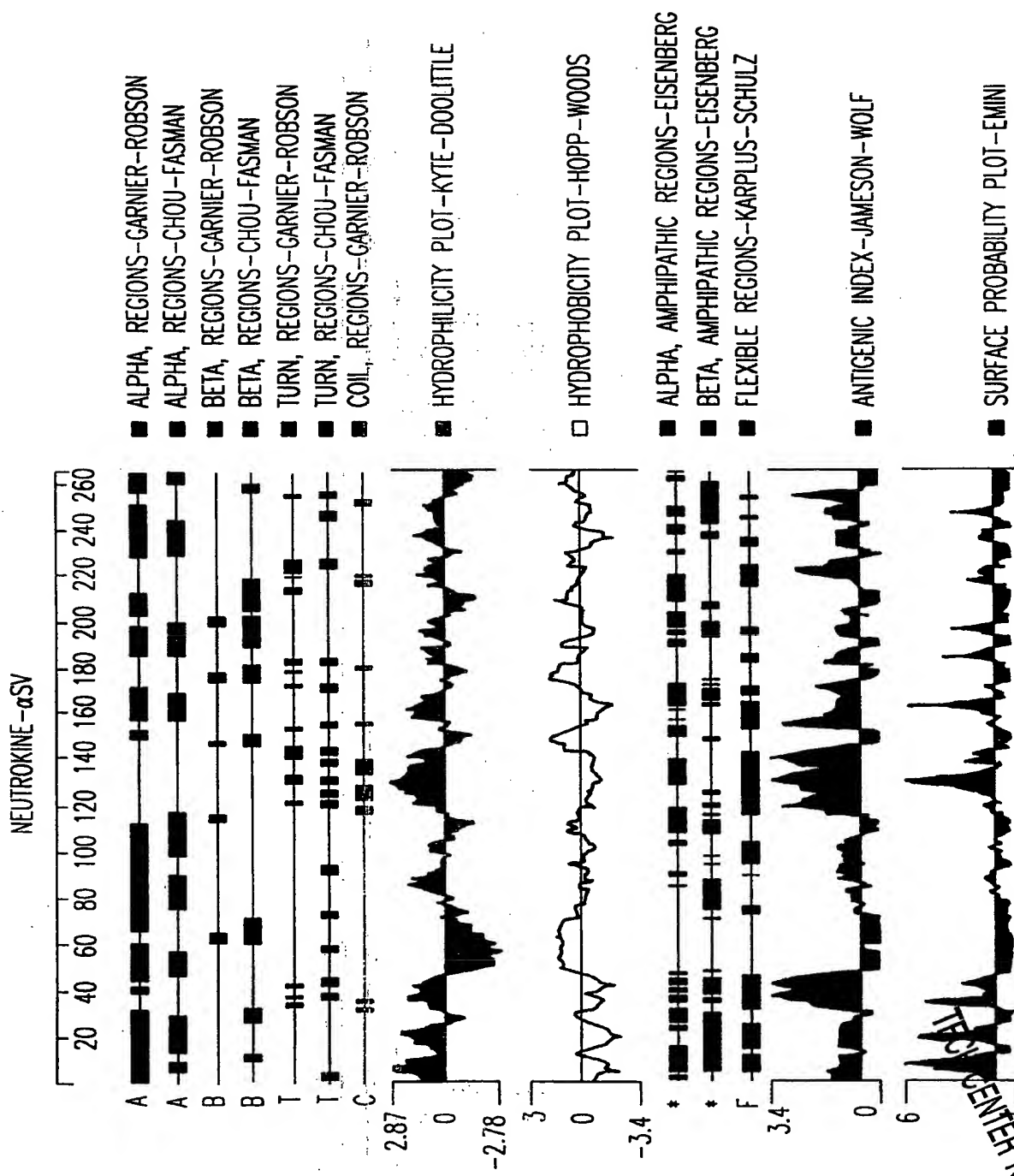
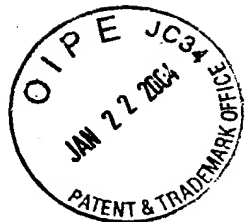


FIG.6

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Neutrokin-

Alpha MDDSTEREQSRLTSCCLKKREEMKLEKCVSILPRKESPSVRS 41

Transmembrane Region

SKDGKLLAATLLALLSCCLTVVSFYQVAALQGDLASLRAE 82

LQGHHAELPAGAGAPKAGLEEAPAVTAGLKIFEPAPGEG 123



A

NSSQNSRNKRAVQGPEETVTQDCQLQLIADSEITPTIQKGSYI 164  
Apr11 HSVLHLLVPINATSK-DDSDVT 134  
TNF KPVAAHVVAANPQAEQG- - - - - 102  
LT α KPAAHLIGDPPSKQNS- - - - - 76

A'

B'

C

FV P W L L S - - - - F K R G S A L E E K E N K I L V K E T G Y F F I Y G Q V L 200  
E V M W Q P A - - - - L R R G R G L Q A Q G Y G V R I Q D A G V Y L L Y S Q V L 170  
- L Q W L N R R A N A L L A N G V E L R D - - N Q L V V P S E G L Y L I Y S Q V L 139  
- L L W R A N T D R A F L Q D G F S L S N - - N S L L V P T S G I Y F V Y S Q V V 114

D

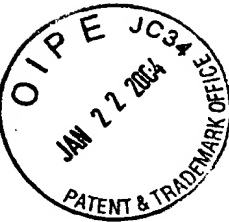
E

Y T D K T Y - - - - A M G H L I Q R K K V H V F G D E L S L V T L F R C I Q N M P 237  
F Q D V T F - - - - T M G Q V V S R E - - - - G Q G R Q E T L F R C I R S M P 201  
F K G Q G C P - - - - S T H V L L T T I S R I A V S Y Q T K V N L L S A I K S P 176  
F V G K A Y S P K A T S S P L Y L A H E V Q L F S S Q V P F H V P L L S S Q K M V 155

FIG.7A-1

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Neutrokin-

Alpha MDDSTEREQSRLTSCCLKREEMKKECVSILPRKESPSVRS 41

Transmembrane Region

SKDGKLLAATLLALLSCCLTVVSFYQVAALQGDLASLRAE 82

LQGHHA EKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEG 123

↓  
NSSQNSRNKRAVQGPEETVTQDCQLQLIADSEPTIQKGSY 164  
April HSVLHLVPIINATSK-DDSDVT 134  
TNF KPVAHVVANPQAEQG- - - - 102  
LT $\alpha$  KPAAHLIGDPPSKQNS- - - - 76

A' B' C  
FVPLLS- - - - FKRGSALEEKENKILVKETGYFFIYGQVL 200  
EVMWQPA- - - - LRRGRGLQAQGYGVRIQDAGVYLLYSQVL 170  
- LQWLNRANALLANGVELRD- - NQLVVPSEGLYLLYSQVL 139  
- LLLRANTDRAFLQDGFSLSN- - NSLLVPTSGIYFVYSQVV 114  
D E  
YTDKTY- - - - AMGHLIQRKKHVFGDELSLVTLFRCIQNMP 237  
FQDVIF- - - - MGQVVSRE- - - - GQGRQETLFRCI RSM 201  
FKGQGPC- - - - STHVLTLTISRIVSVQTKVNLISAISKSP 176  
FSGKAVSPKATSSPLYLAHEVQLFSSQVPFHVPLSSQKM 155

FIG.7A-1

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Neutrokine-

Alpha MDDSTEREQSRLTSCCLKKREEMKLEKCVSILPRKESPSVRS 41

Transmembrane Region

SKDGKLLAATLLALLSCCLTVVSFYQVAALQGDLASLRAE 82

LQGHHAELPAGAGAPKAGLEEAPAVTAGLKIFEPAPGEG 123

A

NSSQNSRNKRAVQGPETVTQDCQLQLIADSEITPTIQKGSY 164  
 April HSVLHLVPINATTSK-DDSDVT 134  
 TNF KPVAAHVVANPQAEQG- - - - - 102  
 LT  $\alpha$  KPAAHLIGDPPSKQNS- - - - - 76

C

B

B'

A'

FVPMLLS- - - - - FKRGSALEEEKEENKILVKETGYFFIYGGQVL 200  
 EVMMQPA- - - - - LRRGRGLQAQGYGVRIQDDAGVYLLYSQVL 170  
 - LQWLNRRANALLANGVELRD- - - NQLVVPSEGLYLLIYSQVL 139  
 - LLWRANTDRALLQDGFSLSN- - - NLLVPTSGIYFVYSQVV 114

D

E

YTDKTY- - - - - AMGHLIQRKKVHVFGDELSLVTLFRCIQNMP 237  
 FQDVTTF- - - - - TMGQVVSRE- - - - - GQGRQETTLFRCIRSM 201  
 FQKGGQGPCP- - - - - STHVLTLTHISRIVSVYQTKVNLLSAISKSP 176  
 FSGKAYSPKATSSPLLALHEVQLFSSQYYPFHVPLLSSQKM 155

FIG.7A-1

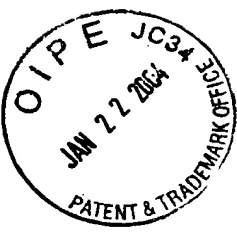
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F										G										H																					
E	-	-	T	L	P	-	-	-	-	-	-	N	N	S	C	Y	S	A	G	I	A	K	L	E	E	G	D	E	L	Q	L	A	I	P	R	E	N	A	268		
S	H	P	D	R	A	-	-	-	-	-	-	Y	N	S	C	Y	S	A	G	V	F	H	L	H	Q	Q	D	I	L	S	V	I	I	P	R	A	R	A	234		
C	Q	R	E	T	P	E	G	A	E	A	K	P	W	Y	E	P	I	Y	L	G	G	V	F	Q	L	E	K	G	D	R	L	S	A	E	I	N	R	P	D	Y	217
Y	P	-	-	-	-	-	G	L	Q	E	P	W	L	H	S	M	Y	H	G	A	A	F	Q	L	T	Q	Q	G	D	Q	L	S	T	H	T	D	G	I	P	H	190
H																																									
Q	I	S	L	D	G	D	V	T	F	F	G	A	L	K	L	L																					285				
K	L	N	L	S	P	H	G	T	F	L	G	F	V	K	L	L																					250				
L	D	F	A	E	S	G	Q	V	Y	F	G	I	I	A	L	L																					233				
L	V	L	S	-	P	S	T	V	F	F	G	A	F	A	L	L																					205				

FIG.7A-2

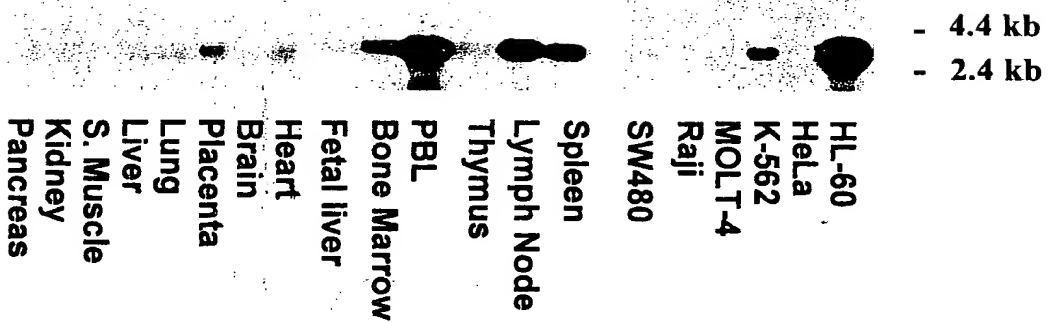
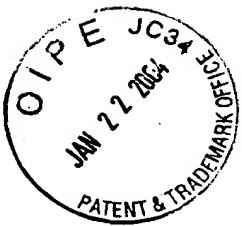


FIG. 7B

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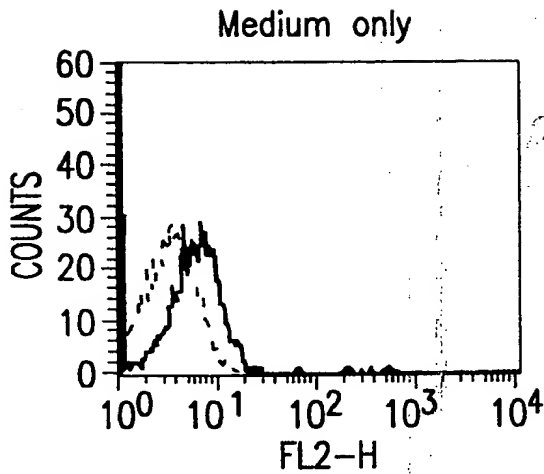


FIG.8A

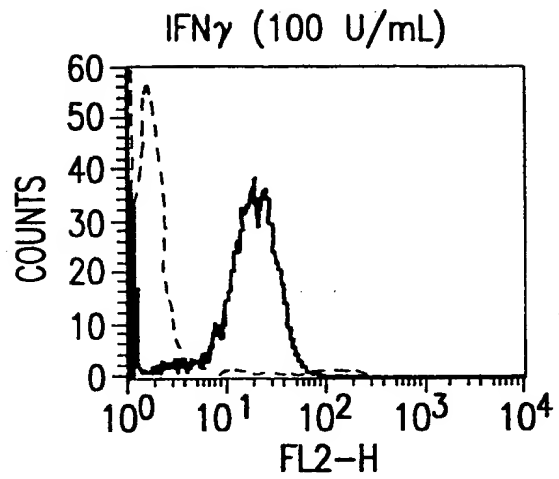


FIG.8B

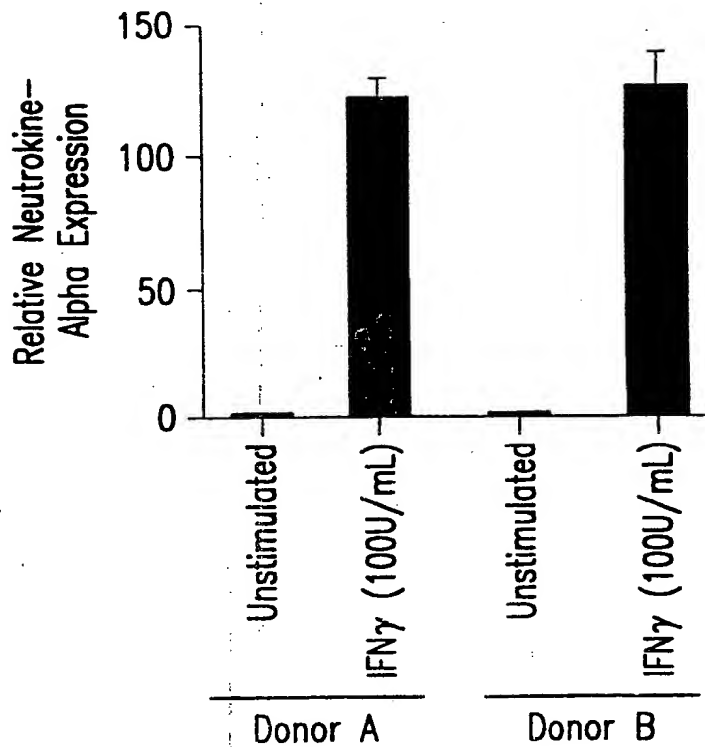


FIG.8C

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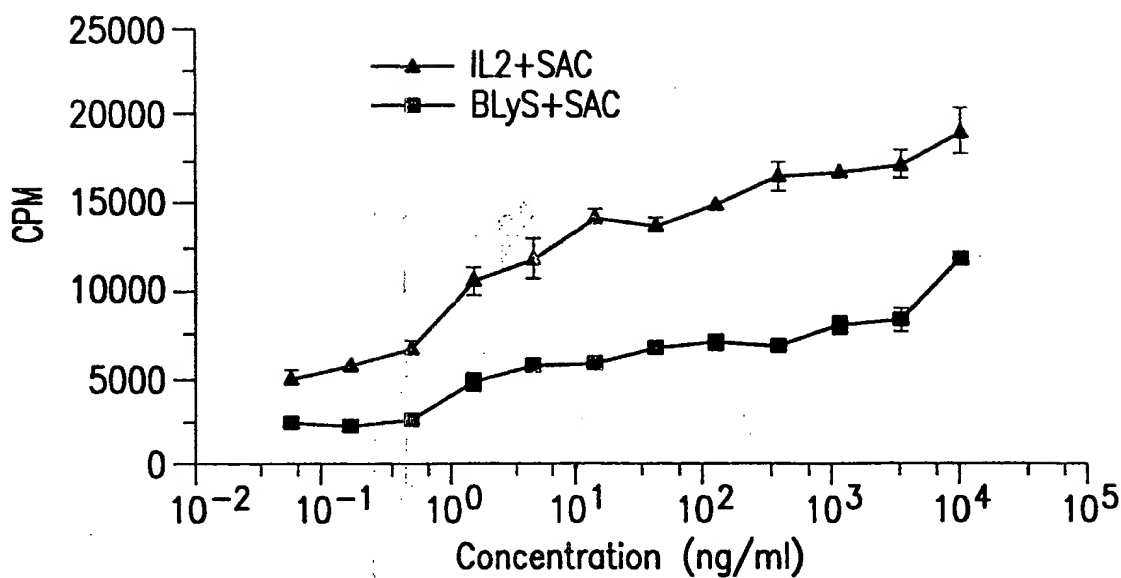


FIG. 9A

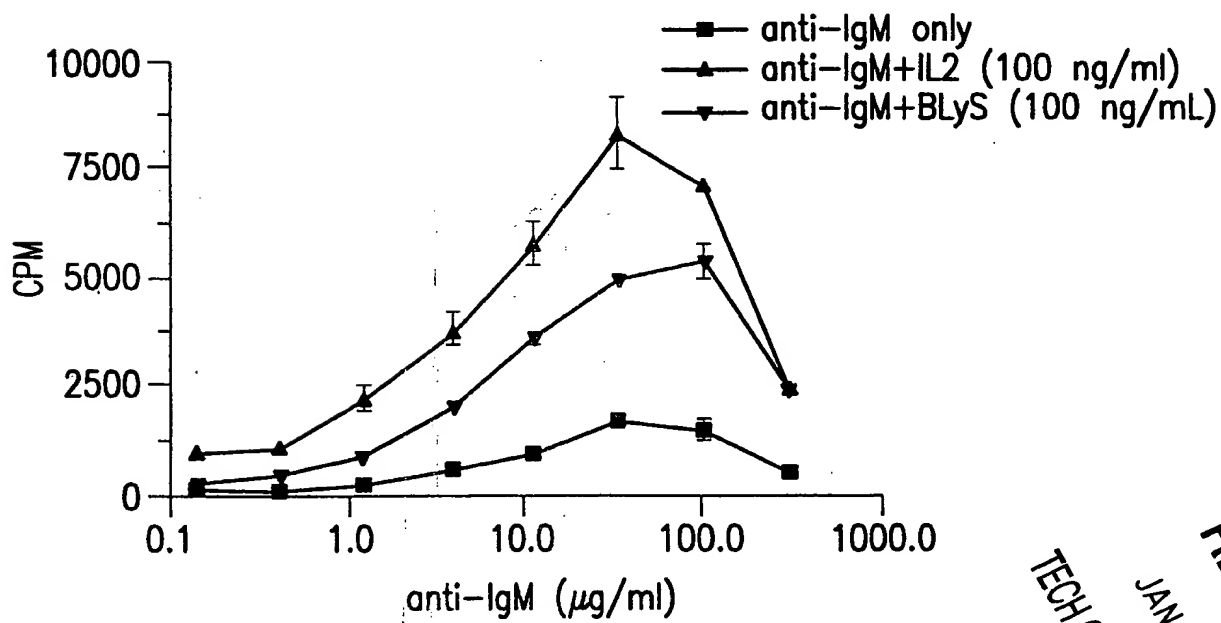


FIG. 9B

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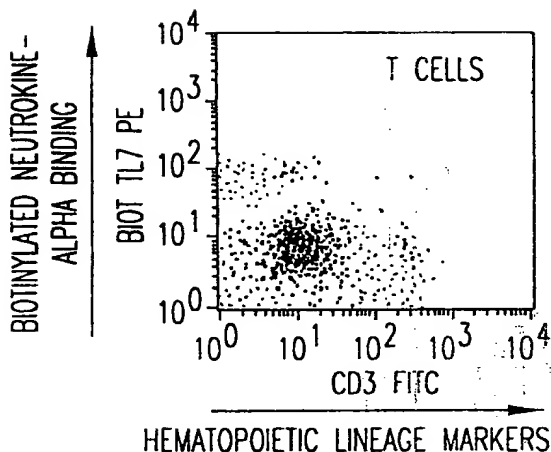
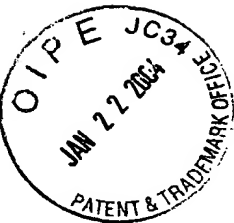


FIG.10A

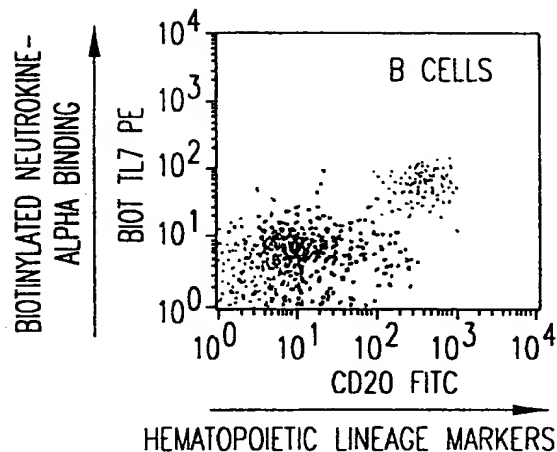


FIG.10B

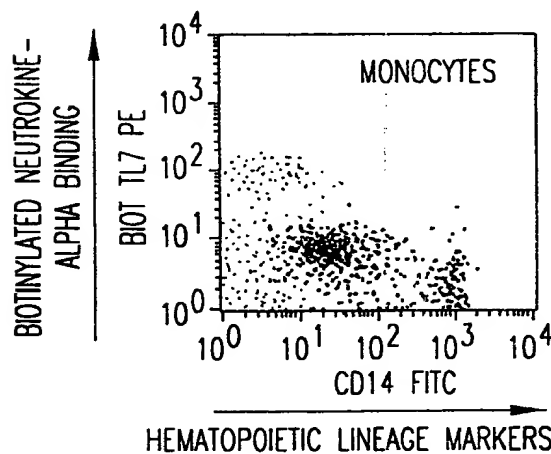


FIG.10C

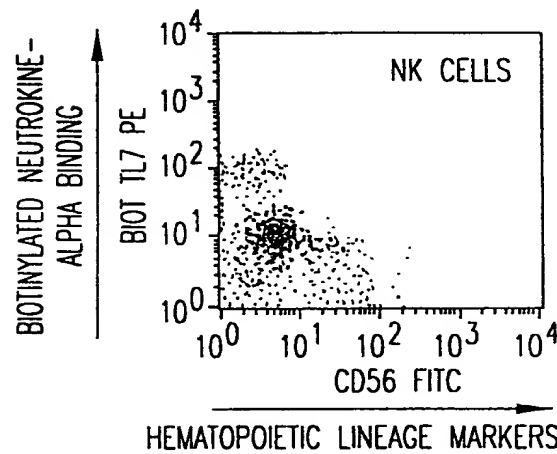


FIG.10D

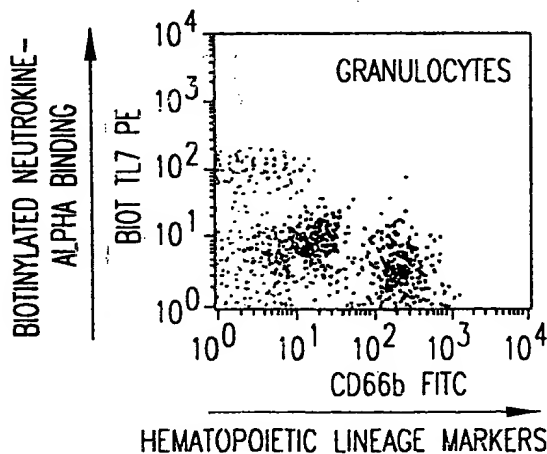


FIG.10E

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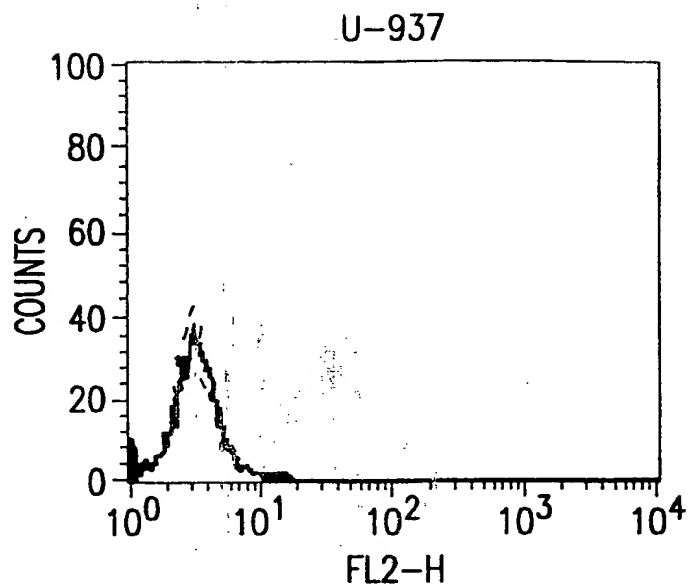
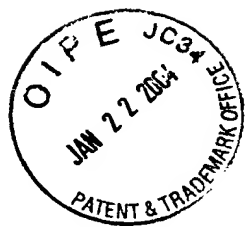


FIG.10F

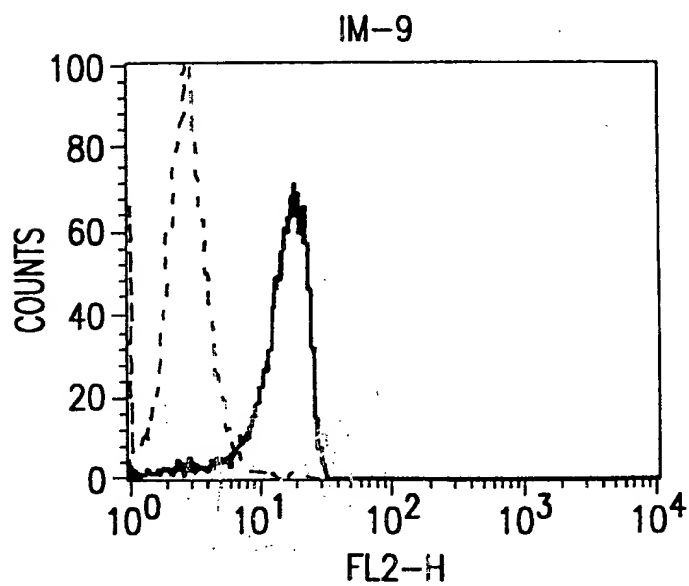


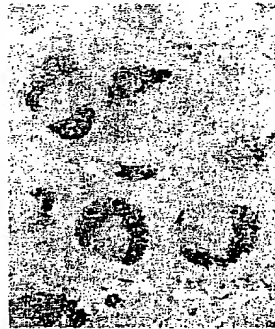
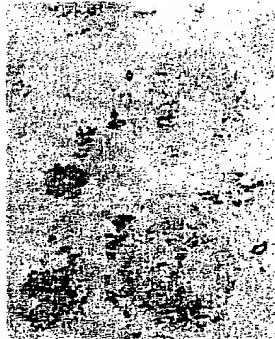
FIG.10G

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Neutrokinine - alpha  
treated spleen  
(2mg/Kg) bid 4d

Normal spleen



H & E (100X)

CD45R(B220)  
(40X)

FIG.11A

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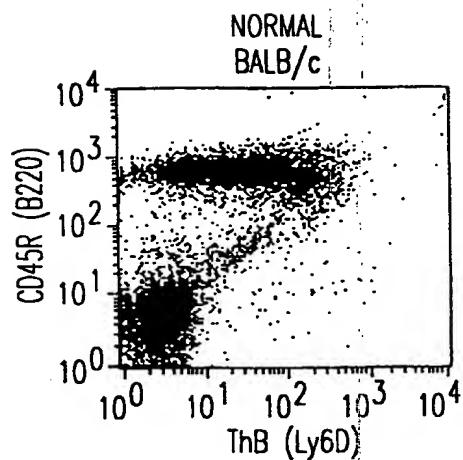


FIG. 11B

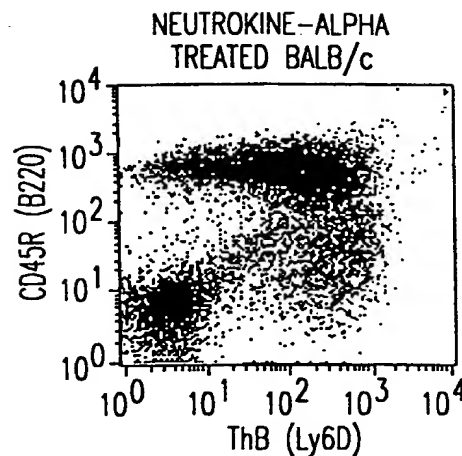


FIG. 11C

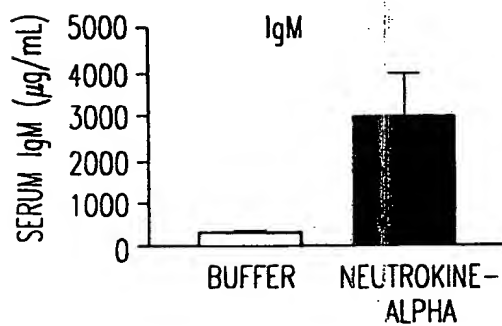


FIG. 11D

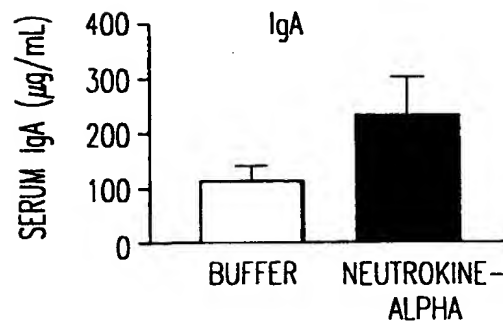


FIG. 11E

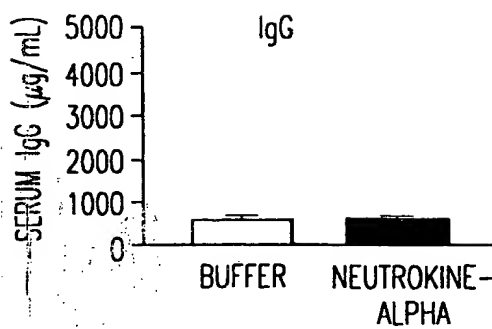


FIG. 11F

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